

10/501071

SEQUENCE LISTING

DT04 Rec'd PCT/PTO 09 JUL 2004

<110> University of Newcastle Upon Tyne

<120> Fusion Proteins

<130> 43952/JMD/MAR

<150> GB 0200689.8

<151> 2002-01-10

<160> 61

<170> PatentIn version 3.1

<210> 1

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Ala3-His6 tail

<400> 1

Ala Ala Ala His His His His His His  
1 5

<210> 2

<211> 25

<212> PRT

<213> Escherichia coli

<400> 2

Met Asn Met Lys Lys Leu Ala Thr Leu Val Ser Ala Val Ala Leu Ser  
1 5 10 15

Ala Thr Val Ser Ala Asn Ala Met Ala  
20 25

<210> 3

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Cleavage site for enterokinase

<400> 3

Asp Asp Asp Asp Lys  
1 5

<210> 4

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Cleavage site for thrombin

<400> 4

Leu Val Pro Arg  
1

<210> 5

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Cleavage site for factor Xa

<400> 5

Ile Glu Gly Arg  
1

<210> 6  
<211> 4  
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<400> 6

His His His His  
1

<210> 7  
<211> 5  
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His His His His His  
1 5

<210> 8  
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His His His His His His  
1 5

<210> 9

<211> 7

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<223> 7xHis tag

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His His His His His His His  
1 5

<210> 10

<211> 8

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<213> Artificial Sequence

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<223> 8xHis tag

<400> 10

His His His His His His His His  
1 5

<210> 11

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> 9xHis tag

<400> 11

His His His His His His His His His  
1 5

<210> 12

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> 10xHis tag

<400> 12

His His His His His His His His His His His  
1 5 10

<210> 13

<211> 93

<212> PRT

<213> Escherichia coli

<400> 13

Asn Asn Gly Ala Ser Gly Ala Asp Ile Asn Asn Tyr Ala Gly Gln Ile  
1 5 10 15

Lys Ser Ala Ile Glu Ser Lys Phe Tyr Asp Ala Ser Ser Tyr Ala Gly  
20 25 30

Lys Thr Cys Thr Leu Arg Ile Lys Leu Ala Pro Asp Gly Met Leu Leu  
35 40 45

Asp Ile Lys Pro Glu Gly Gly Asp Pro Ala Leu Cys Gln Ala Ala Leu  
50 55 60

Ala Ala Ala Lys Leu Ala Lys Ile Pro Lys Pro Pro Ser Gln Ala Val  
65 70 75 80

Tyr Glu Val Phe Lys Asn Ala Pro Leu Asp Phe Lys Pro  
85 90

<210> 14

<211> 348

<212> PRT

<213> Artificial Sequence

<220>

<223> TolA-BCL fusion protein

<400> 14

Met His His His His His His Ser Ser Asn Asn Gly Ala Ser Gly Ala  
1 5 10 15

Asp Ile Asn Asn Tyr Ala Gly Gln Ile Lys Ser Ala Ile Glu Ser Lys  
20 25 30

Phe Tyr Asp Ala Ser Ser Tyr Ala Gly Lys Thr Cys Thr Leu Arg Ile  
35 40 45

Lys Leu Ala Pro Asp Gly Met Leu Leu Asp Ile Lys Pro Glu Gly Gly  
50 55 60

Asp Pro Ala Leu Cys Gln Ala Ala Leu Ala Ala Ala Lys Leu Ala Lys  
65 70 75 80

Ile Pro Lys Pro Pro Ser Gln Ala Val Tyr Glu Val Phe Lys Asn Ala  
85 90 95

Pro Leu Asp Phe Lys Pro Gly Gly Gly Ser Gly Ser Leu Val Pro Arg  
100 105 110

Gly Ser Arg Pro Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu  
115 120 125

Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp  
130 135 140

Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met  
145 150 155 160

Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp  
165 170 175

Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp Ala  
180 185 190

Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala  
195 200 205

Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr  
210 215 220

Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln  
225 230 235 240

Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val  
245 250 255

Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys  
260 265 270

Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr Tyr  
275 280 285

Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp  
290 295 300

Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys  
305 310 315 320

Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val Ala  
325 330 335

Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys  
340 345

<210> 15

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> To1A-BCL fusion protein after thrombin cleavage

<400> 15

Gly Ser Arg Pro Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu  
1 5 10 15

Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp  
20 25 30

Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met  
35 40 45

Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp  
50 55 60

Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp Ala  
65 70 75 80

Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala  
85 90 95

Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr  
                   100                                  105                                  110  
 Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln  
                   115                                  120                                  125  
 Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val  
                   130                                  135                                  140  
 Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys  
                   145                                  150                                  155                                  160  
 Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr Tyr  
                   165                                  170                                  175  
 Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp  
                   180                                  185                                  190  
 Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys  
                   195                                  200                                  205  
 Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val Ala  
                   210                                  215                                  220  
 Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys  
                   225                                  230                                  235

<210> 16

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Tagged TolAIII region of pTol vectors

<220>

<221> MISC\_FEATURE

<222> (107)..(111)

<223> xaa residues represent cleavage sites DDDDK (SEQ ID NO: 3), LVPR  
 (SEQ ID NO: 4; no Xaa at position 111) or IEGR (SEQ ID NO: 5; no  
 xaa at position 111)



<400> 16

Met His His His His His His Ser Ser Asn Asn Gly Ala Ser Gly Ala  
1 5 10 15

Asp Ile Asn Asn Tyr Ala Gly Gln Ile Lys Ser Ala Ile Glu Ser Lys  
20 25 30

Phe Tyr Asp Ala Ser Ser Tyr Ala Gly Lys Thr Cys Thr Leu Arg Ile  
35 40 45

Lys Leu Ala Pro Asp Gly Met Leu Leu Asp Ile Lys Pro Glu Gly Gly  
50 55 60

Asp Pro Ala Leu Cys Gln Ala Ala Leu Ala Ala Ala Lys Leu Ala Lys  
65 70 75 80

Ile Pro Lys Pro Pro Ser Gln Ala Val Tyr Glu Val Phe Lys Asn Ala  
85 90 95

Pro Leu Asp Phe Lys Pro Gly Gly Gly Ser Xaa Xaa Xaa Xaa Xaa Gly  
100 105 110

Ser Gly Thr  
115

<210> 17

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> His6-Ser2 linker

<400> 17

His His His His His His Ser Ser  
1 5

<210> 18

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> short flexible polypeptide

<400> 18

Gly Gly Gly Ser  
1

<210> 19

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> cleavage/cloning site of pTolE vector

<400> 19

ggtgggggat ctgatgatga cgataaagga tccggtacct gatgaacgcg t 51

<210> 20

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> cleavage/cloning site of pTolT vector

<400> 20

ggtgggggat ctctggttcc gcgcggatcc ggtacctgat gaacgcgt 48

<210> 21

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> cleavage/cloning site of pTolX vector

<400> 21

ggtgggggat ctattgaagg tcgcggatcc ggtacctgat gaacgcgt 48

<210> 22

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Cleavage/cloning site of pTolE vector

<220>

<221> MISC\_FEATURE

<222> (14)..(15)

<223> Xaa represents stop codon site

<400> 22

Gly Gly Gly Ser Asp Asp Asp Asp Lys Gly Ser Gly Thr Xaa Xaa Thr  
1 5 10 15

Arg

<210> 23

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Cleavage/cloning site of pTolT vector

<220>

<221> MISC\_FEATURE

<222> (13)..(14)

<223> Xaa represents stop codon site

<400> 23

Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Thr Xaa Xaa Thr Arg  
1 5 10 15

<210> 24  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> cleavage/cloning site of pTolX vector  
<220>  
<221> MISC\_FEATURE  
<222> (13)..(14)  
<223> Xaa represents stop codon site

<400> 24  
Gly Gly Gly Ser Ile Glu Gly Arg Gly Ser Gly Thr Xaa Xaa Thr Arg  
1 5 10 15

<210> 25  
<211> 2  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gly-Ser tag  
<400> 25

Gly Ser  
1

<210> 26  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gly-Ser-Gly-Thr tag

<400> 26

Gly Ser Gly Thr  
1

<210> 27

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 27  
gatctgatga tgacgataaa ggatccgga cctgatgaa 39

<210> 28

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 28  
cgcggtcatc aggtaccgga tcctttatcg tcatcatca 39

<210> 29

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 29  
gatctattga aggtcgcgga tccggtacct gatgaa 36

<210> 30

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 30

cgcggtcatc aggtaccgga tccgcgacct tcaata

36

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 31

gatctctggt tccgcgcgga tccggtacct gatgaa

36

<210> 32

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 32

cgcggtcatc aggtaccgga tccgcgcgga accaga

36

<210> 33

<211> 37

<212> PRT

<213> Escherichia coli

<400> 33

Asn Ser Asn Gly Trp Ser Trp Ser Asn Lys Pro His Lys Asn Asp Gly  
1 5 10 15

Phe His Ser Asp Gly Ser Tyr His Ile Thr Phe His Gly Asp Asn Asn  
20 25 30

Ser Lys Pro Lys Pro  
35

<210> 34

<211> 80

<212> PRT

<213> Escherichia coli

<400> 34

Asn Asn Ala Phe Gly Gly Gly Lys Asn Pro Gly Ile Gly Asn Thr Ser  
1 5 10 15

Gly Ala Gly Ser Asn Gly Ser Ala Ser Ser Asn Arg Gly Asn Ser Asn  
20 25 30

Gly Trp Ser Trp Ser Asn Lys Pro His Lys Asn Asp Gly Phe His Ser  
35 40 45

Asp Gly Ser Tyr His Ile Thr Phe His Gly Asp Asn Asn Ser Lys Pro  
50 55 60

Lys Pro Gly Gly Asn Ser Gly Asn Arg Gly Asn Asn Gly Asp Gly Ala  
65 70 75 80

<210> 35

<211> 117

<212> PRT

<213> Escherichia coli

<400> 35

His Gly Asp Asn Asn Ser Lys Pro Lys Pro Gly Gly Asn Ser Gly Asn  
1 5 10 15

Arg Gly Asn Asn Gly Asp Gly Ala Ser Ala Lys Val Gly Glu Ile Thr  
20 25 30

Ile Thr Pro Asp Asn Ser Lys Pro Gly Arg Tyr Ile Ser Ser Asn Pro  
35 40 45

Glu Tyr Ser Leu Leu Ala Lys Leu Ile Asp Ala Glu Ser Ile Lys Gly  
50 55 60

Thr Glu Val Tyr Thr Phe His Thr Arg Lys Gly Gln Tyr Val Lys Val  
65 70 75 80

Thr Val Pro Asp Ser Asn Ile Asp Lys Met Arg Val Asp Tyr Val Asn  
85 90 95

Trp Lys Gly Pro Lys Tyr Asn Asn Lys Leu Val Lys Arg Phe Val Ser  
100 105 110

Gln Phe Leu Leu Phe  
115

<210> 36

<211> 124

<212> PRT

<213> Homo sapiens

<400> 36

Asn Leu Val Asn Phe His Arg Met Ile Lys Leu Thr Thr Gly Lys Glu  
1 5 10 15

Ala Ala Leu Ser Tyr Gly Phe Tyr Gly Cys His Cys Gly Val Gly Gly  
20 25 30

Arg Gly Ser Pro Lys Asp Ala Thr Asp Arg Cys Cys Val Thr His Asp  
35 40 45

Cys Cys Tyr Lys Arg Leu Glu Lys Arg Gly Cys Gly Thr Lys Phe Leu  
50 55 60

Ser Tyr Lys Phe Ser Asn Ser Gly Ser Arg Ile Thr Cys Ala Lys Gln  
65 70 75 80

Asp Ser Cys Arg Ser Gln Leu Cys Glu Cys Asp Lys Ala Ala Ala Thr  
85 90 95

Cys Phe Ala Arg Asn Lys Thr Thr Tyr Asn Lys Lys Tyr Gln Tyr Tyr  
100 105 110

Ser Asn Lys His Cys Arg Gly Ser Thr Pro Arg Cys  
115 120



<210> 37

<211> 179

<212> PRT

<213> Actinia equina

<400> 37

Ser Ala Asp Val Ala Gly Ala Val Ile Asp Gly Ala Ser Leu Ser Phe  
1 5 10 15

Asp Ile Leu Lys Thr Val Leu Glu Ala Leu Gly Asn Val Lys Arg Lys  
20 25 30

Ile Ala Val Gly Val Asp Asn Glu Ser Gly Lys Thr Trp Thr Ala Leu  
35 40 45

Asn Thr Tyr Phe Arg Ser Gly Thr Ser Asp Ile Val Leu Pro His Lys  
50 55 60

Val Pro His Gly Lys Ala Leu Leu Tyr Asn Gly Gln Lys Asp Arg Gly  
65 70 75 80

Pro Val Ala Thr Gly Ala Val Gly Val Leu Ala Tyr Leu Met Ser Asp  
85 90 95

Gly Asn Thr Leu Ala Val Leu Phe Ser Val Pro Tyr Asp Tyr Asn Trp  
100 105 110

Tyr Ser Asn Trp Trp Asn Val Arg Ile Tyr Lys Gly Lys Arg Arg Ala  
115 120 125

Asp Gln Arg Met Tyr Glu Glu Leu Tyr Tyr Asn Leu Ser Pro Phe Arg  
130 135 140

Gly Asp Asn Gly Trp His Thr Arg Asn Leu Gly Tyr Gly Leu Lys Ser  
145 150 155 160

Arg Gly Phe Met Asn Ser Ser Gly His Ala Ile Leu Glu Ile His Val  
165 170 175

Ser Lys Ala

<210> 38

<211> 191

<212> PRT

<213> Homo sapiens

<400> 38

Thr Gly Ala Gly Lys Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu  
1 5 10 15

Glu Pro Ser Glu Gly Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys  
20 25 30

Ser Gln Phe Ser Trp Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile  
35 40 45

Phe Gly Val Ser Tyr Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala  
50 55 60

Cys Gln Leu Glu Glu Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile  
65 70 75 80

Val Leu Gly Glu Gly Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg  
85 90 95

Ile Ser Leu Ala Arg Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu  
100 105 110

Asp Ser Pro Phe Gly Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe  
115 120 125

Glu Ser Cys Val Cys Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val  
130 135 140

Thr Ser Lys Met Glu His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu  
145 150 155 160

His Glu Gly Ser Ser Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn  
165 170 175

Leu Gln Pro Asp Phe Ser Ser Lys Leu Met Gly Cys Asp Ser Phe  
180 185 190

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Lys Tyr Ile Glu His Phe Ser Lys Phe Ser Pro Ser Pro Leu Ser Met  
1 5 10 15

Lys Gln Phe Leu Asp Phe Gly Ser Ser Asn Ala Cys Glu Lys Thr Ser  
20 25 30

Phe Thr Phe Leu Arg Gln Glu Leu Pro Val Arg Leu Ala Asn Ile Met  
35 40 45

Lys Glu Ile Asn Leu Leu Pro Asp Arg Val Leu Ser Thr Pro Ser Val  
50 55 60

Gln Leu Val Gln Ser Trp Tyr Val Gln Ser Leu Leu Asp Ile Met Glu  
65 70 75 80

Phe Leu Asp Lys Asp Pro Glu Asp His Arg Thr Leu Ser Gln Phe Thr  
85 90 95

Asp Ala Leu Val Thr Ile Arg Asn Arg His Asn Asp Val Val Pro Thr  
100 105 110

Met Ala Gln Gly Val Leu Glu Tyr Lys Asp Thr Tyr Gly Asp Asp Pro  
115 120 125

Val Ser Asn Gln Asn Ile Gln Tyr Phe Leu Asp Arg Phe Tyr Leu Ser  
130 135 140

Arg Ile Ser Ile Arg Met Leu Ile Asn Gln His Thr Leu Ile Phe Asp  
145 150 155 160

Gly Ser Thr Asn Pro Ala His Pro Lys His Ile Gly Ser Ile Asp Pro  
165 170 175

Asn Cys Asn Val Ser Glu Val Val Lys Asp Ala Tyr Asp Met Ala Lys  
180 185 190

Leu Leu Cys Asp Lys Tyr Tyr Met Ala Ser Pro Asp Leu Glu Ile Gln  
195 200 205

Glu Ile Asn Ala Ala Asn Ser Lys Gln Pro Ile His Met Val Tyr Val  
210 215 220

Pro Ser His Leu Tyr His Met Leu Phe Glu Leu Phe Lys Asn Ala Met  
225 230 235 240

Arg Ala Thr Val Glu Ser His Glu Ser Ser Leu Ile Leu Pro Pro Ile  
245 250 255

Lys Val Met Val Ala Leu Gly Glu Glu Asp Leu Ser Ile Lys Met Ser  
260 265 270

Asp Arg Gly Gly Gly Val Pro Leu Arg Lys Ile Glu Arg Leu Phe Ser  
275 280 285

Tyr Met Tyr Ser Thr Ala Pro Thr Pro Gln Pro Gly Thr Gly Gly Thr  
290 295 300

Pro Leu Ala Gly Phe Gly Tyr Gly Leu Pro Ile Ser Arg Leu Tyr Ala  
305 310 315 320

Lys Tyr Phe Gln Gly Asp Leu Gln Leu Phe Ser Met Glu Gly Phe Gly  
325 330 335

Thr Asp Ala Val Ile Tyr Leu Lys Ala Leu Ser Thr Asp Ser Val Glu  
340 345 350

Arg Leu Pro Val Tyr Asn Lys Ser Ala Trp Arg His Tyr Gln Thr Ile  
355 360 365

Gln Glu Ala Gly Asp Trp Cys Val Pro Ser Thr Glu Pro Lys Asn Thr  
370 375 380

Ser Thr Tyr Arg Val Ser  
385 390

<210> 40

<211> 202

<212> PRT

<213> Bacillus licheniformis

<400> 40

Ser Phe Ser Glu Leu Asn Ile Asp Ala Phe Arg Phe Ile Asn Asp Leu  
1 5 10 15

Gly Lys Glu Tyr Ser Met Leu Asn Pro Val Val Tyr Phe Leu Ala Glu  
20 25 30

Tyr Met Met Tyr Phe Leu Ala Leu Gly Leu Val Val Tyr Trp Leu Thr  
35 40 45

Arg Thr Thr Lys Asn Arg Leu Met Val Ile Tyr Ala Val Ile Ala Phe  
50 55 60

Val Val Ala Glu Ile Leu Gly Lys Ile Met Gly Ser Leu His Ser Asn  
65 70 75 80

Tyr Gln Pro Phe Ala Thr Leu Pro Asn Val Asn Lys Leu Ile Glu His  
85 90 95

Glu Ile Asp Asn Ser Phe Pro Ser Asp His Thr Ile Leu Phe Phe Ser  
100 105 110

Ile Gly Phe Leu Ile Phe Leu Phe His Lys Lys Thr Gly Trp Leu Trp  
115 120 125

Leu Val Leu Ala Phe Ala Val Gly Ile Ser Arg Ile Trp Ser Gly Val  
130 135 140

His Tyr Pro Leu Asp Val Ala Ala Gly Ala Leu Leu Gly Val Leu Ser  
145 150 155 160

Ala Leu Phe Val Phe Trp Thr Ala Pro Lys Leu Ser Phe Ile His Gln  
165 170 175

Met Leu Ser Leu Tyr Glu Lys Val Glu Gln Arg Ile Val Pro Ser Lys  
180 185 190

Asn Lys Ser Asn Asp Lys Ser Lys Asn Phe  
195 200

<210> 41

<211> 354

<212> PRT

<213> Homo sapiens

<400> 41

Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser Lys Leu Phe Phe  
1 5 10 15

Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg Gln Arg Leu Glu  
20 25 30

Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser Ala Asp Asn Leu  
35 40 45

Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu Ala Ser Lys Lys  
50 55 60

Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg Phe  
65 70 75 80

Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala Val  
85 90 95

Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr Asp Pro Asp Asn  
100 105 110

Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys Leu  
115 120 125

Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala Ile Phe Gly Leu  
130 135 140

His His Ile Gly Met Gln Met Arg Ile Ala Met Phe Ser Leu Ile Tyr  
145 150 155 160

Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser Ile  
165 170 175

Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp Glu  
180 185 190

Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val Ala  
195 200 205

Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe Cys  
210 215 220

Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu Gly  
225 230 235 240

Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly Lys Ile Ser Glu  
245 250 255

Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile Gln Ser Val Lys  
260 265 270

Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile Glu Asn Leu Arg  
275 280 285

Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr Val Arg Tyr Phe  
290 295 300

Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val Val Phe Leu Ser  
 305 310 315 320

Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu Arg Lys Ile Phe  
 325 330 335

Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala Val Thr Arg Gln  
 340 345 350

Phe Pro

<210> 42

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 42

tttttgatc caattccaat ggatgggtcat ggag

34

<210> 43

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 43

aaggatccaa gcttcaaggt ttaggctttg aattattgtc c

41

<210> 44

<211> 36

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide  
 <400> 44  
 tttttggatc caatgctttt ggtggaggga aaaatc 36  
  
 <210> 45  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide  
 <400> 45  
 ctcagcgggtg gcagcagcc 19  
  
 <210> 46  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide  
 <400> 46  
 cgcggatccc atggggacaa taattcaaag c 31  
  
 <210> 47  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide  
 <400> 47  
 ggcgaattca cgcgttaaaa taataatttc tggctcac 38  
  
 <210> 48



<211> 37  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide  
 <400> 48  
 ccgggtacc aatttgggtga atttccacag aatgatc 37  
  
 <210> 49  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide  
 <400> 49  
 ggccaattca cgcgttagca acgaggggtg ctccc 35  
  
 <210> 50  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide  
 <400> 50  
 cgcgatccg cagacgtggc tggcgcc 27  
  
 <210> 51  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Synthetic oligonucleotide

<400> 51

ggcgaattca cgcgttaagc tttgctcacg tgagtttc

38

<210> 52

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 52

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